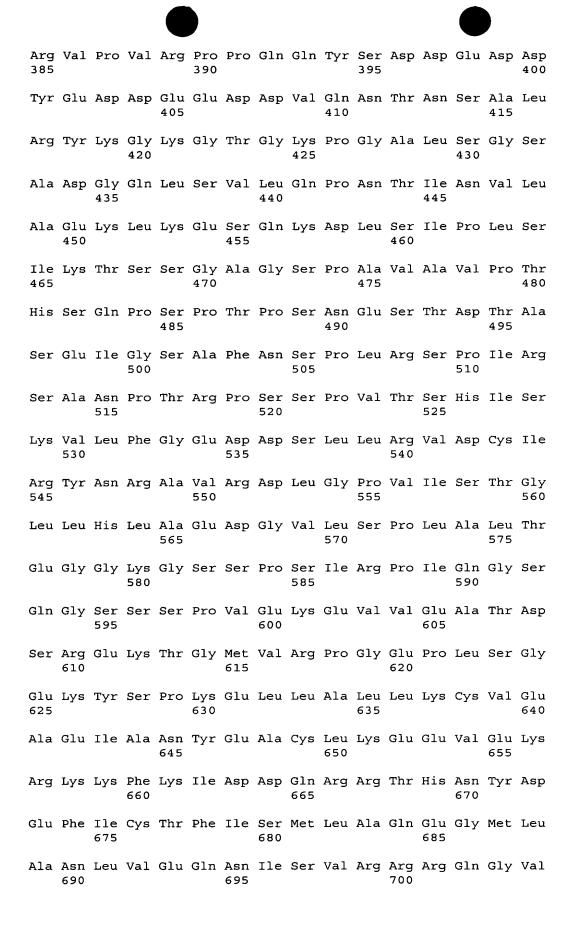
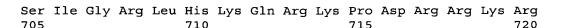
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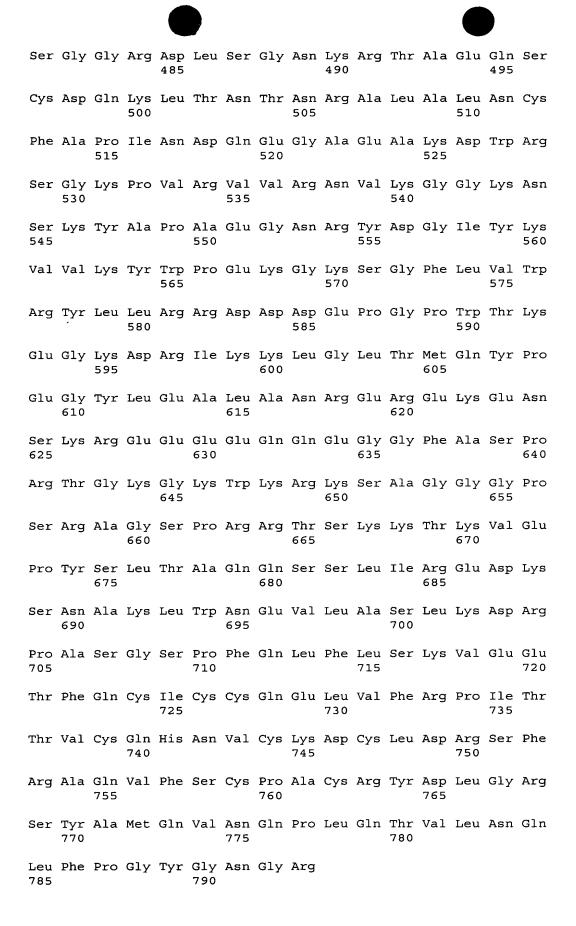
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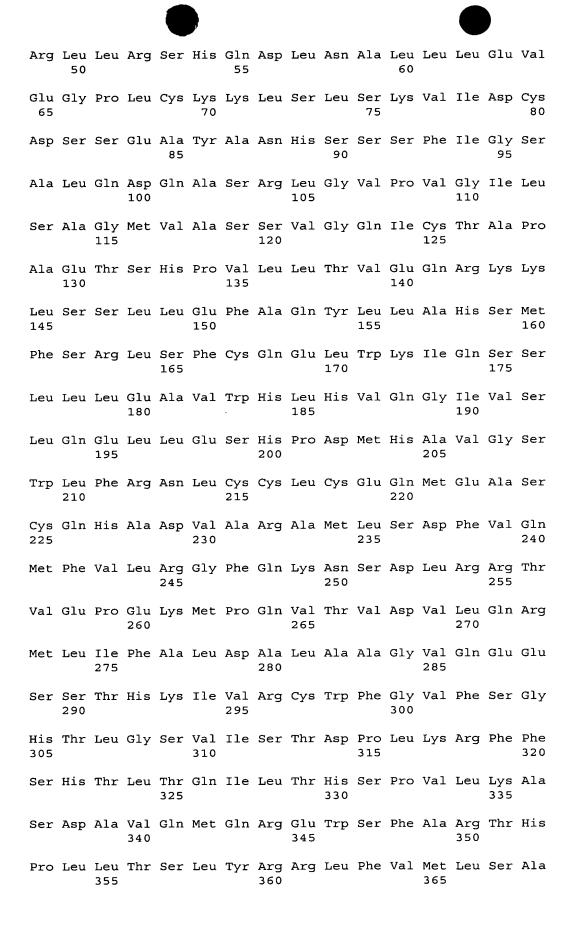
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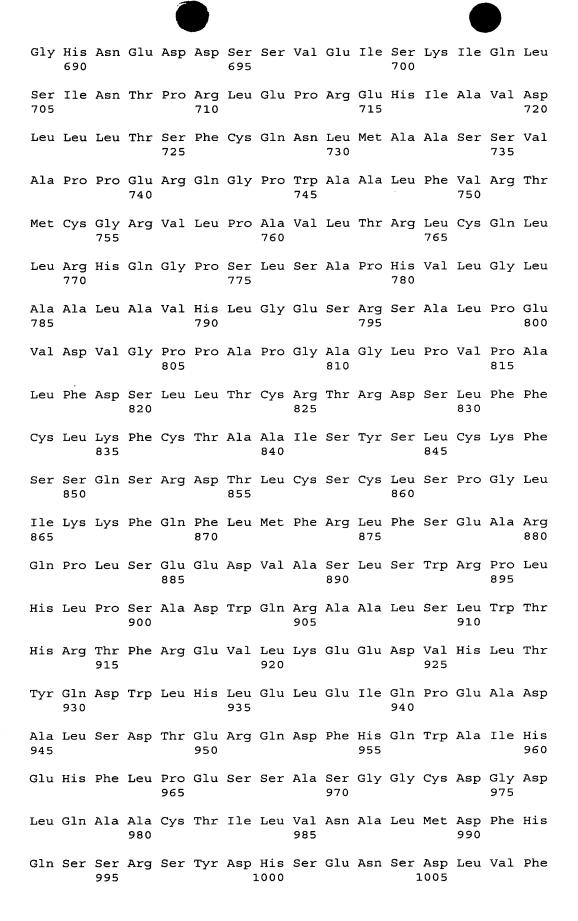
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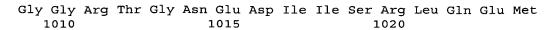
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His Trp Gl 385	n Arg Val	Leu Ser 390	Phe V	al Ser	Ala Le 395	u Val	Val	Cys	Phe 400
Pro Glu Al	a Gln Gln 405		Glu A	sp Trp 410	Val Al	a Arg	Leu	Met 415	Ala
Gln Ala Ph	e Glu Ser 420	Cys Gln		sp Ser 25	Met Va	l Thr	Ala 430	Phe	Leu
Val Val Ar 43	_	Ala Leu	Glu G 440	ly Pro	Ser Al	a Phe 445	Leu	Ser	Tyr
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Val Pro Ph	e Glu Ser 485	_	Tyr L	eu Gln 490	Val Hi	s Ile	Leu	His 495	Pro
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Cys Glu Gln Phe Phe His Leu Val Asn Ser Glu Met Arg Asn Phe Cys 1105 1110 1115 1120

Ser His Gly Gly Ala Leu Thr Gln Asp Ile Thr Ala His Phe Phe Arg 1125 1130 1135

Gly Leu Leu Asn Ala Cys Leu Arg Ser Arg Asp Pro Ser Leu Met Val 1140 1145 1150

Asp Phe Ile Leu Ala Lys Cys Gln Thr Lys Cys Pro Leu Ile Leu Thr 1155 1160 1165

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Trp Arg Arg His Cys Gln Ser Pro Leu Pro Arg Glu Leu Gln Lys Leu 1185 1190 1195 1200

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Ser Pro Ala Pro Asn Pro Asp Trp Leu Ser Ala Ala Ala Leu His Phe 1220 1225 1230

Ala Ile Gln Gln Val Arg Glu Glu Asn Ile Arg Lys Gln Leu Lys Lys 1235 1240 1245

Leu Asp Cys Glu Arg Glu Glu Leu Leu Val Phe Leu Phe Phe Ser 1250 1255 1260

Leu Met Gly Leu Leu Ser Ser His Leu Thr Ser Asn Ser Thr Thr Asp 1265 1270 1275 1280

Leu Pro Lys Ala Phe His Val Cys Ala Ala Ile Leu Glu Cys Leu Glu 1285 1290 1295

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Val Asp Asp Trp Ile Lys Leu Gln Ile Ser His Glu Ala Ala Ala Cys
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Ile Thr Gly Leu Arg Ala Ala Met Glu Ala Leu Val Val Glu Val Thr 65 70 75 80

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Ala Gly Val Gly Gly Gly Tyr Arg Gly Val Ser Arg Gly Gly Phe Arg
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Gly Asn Ser Gly Gly Asp Tyr Arg Gly Pro Ser Gly Gly Tyr Arg Gly
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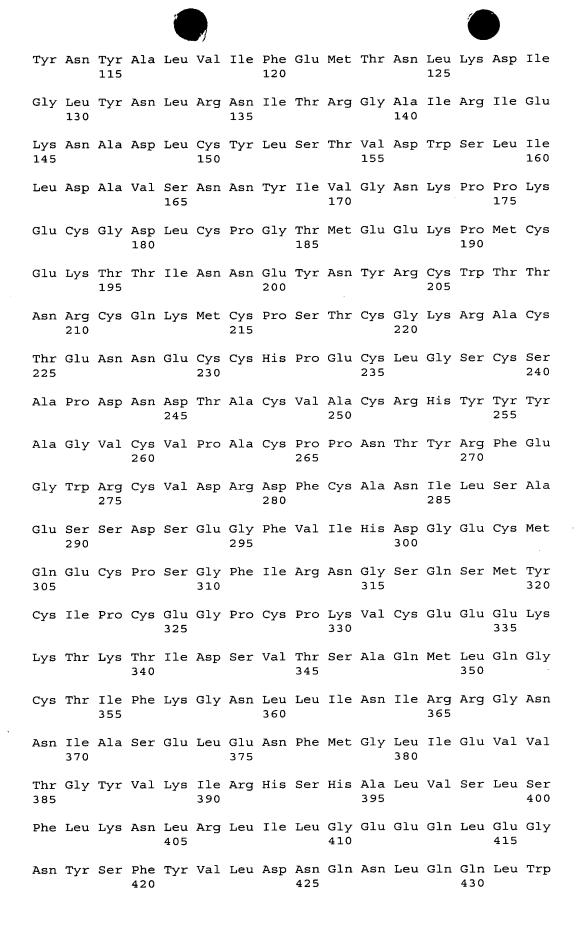


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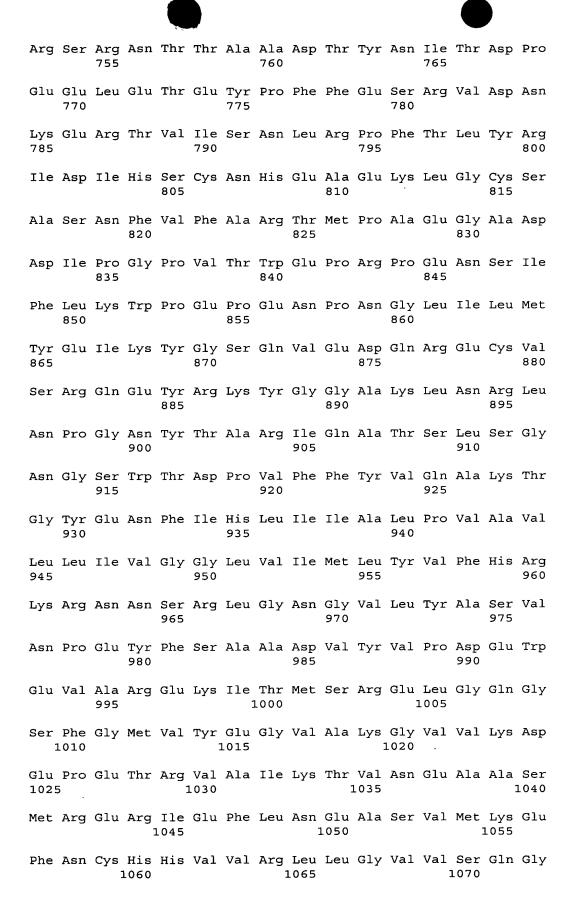


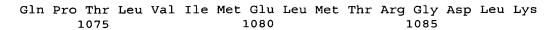
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Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
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Ala Pro Pro Ser Leu Ser Lys Met Ile Gln Met Ala Gly Glu Ile Ala 1105 1110 1115 1120

Asp Gly Met Ala Tyr Leu Asn Ala Asn Lys Phe Val His Arg Asp Leu 1125 1130 1135

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Lys Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys 1235 1240 1245

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Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg Glu Val Ser Phe Tyr 1265 1270 1275 1280

Tyr Ser Glu Glu Asn Lys Leu Pro Glu Pro Glu Glu Leu Asp Leu Glu 1285 1290 1295

Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser Ala Ser Ser Ser 1300 1305 1310

Ser Leu Pro Leu Pro Asp Arg His Ser Gly His Lys Ala Glu Asn Gly 1315 1320 1325

Pro Gly Pro Gly Val Leu Val Leu Arg Ala Ser Phe Asp Glu Arg Gln 1330 1335 1340

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Trp Val Thr Leu Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His
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His Arg Ile His His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr 65 70 75 80

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Asp Asp Glu Asp Met Thr Leu Thr Arg Trp Thr Gly Met Ile Ile Gly 115 120 125

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Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro Phe Val Arg Phe Val Thr
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Lys Ile Asn Met Asn Gly Val Asn Ser Ser Asn Gly Val Val Asp Pro 165 170 175

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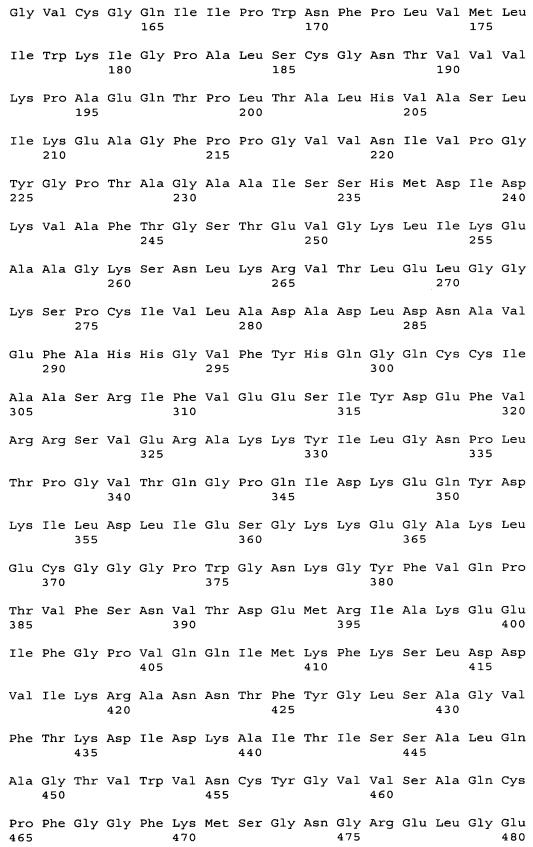
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Ile Pro Ile Asp Gly Asn Phe Phe Thr Tyr Thr Arg His Glu Pro Ile

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Ser Gln Lys Asn Ser 500

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Leu Asp Ile Asp Ser Pro Pro Ile Thr Ala Arg Asn Thr Gly Ile Ile
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Cys Thr Ile Gly Pro Ala Ser Arg Ser Val Glu Thr Leu Lys Glu Met 50 55 60

Ile Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr
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His Glu Tyr His Ala Glu Thr Ile Lys Asn Val Arg Thr Ala Thr Glu 85 90 95

Ser Phe Ala Ser Asp Pro Ile Leu Tyr Arg Pro Val Ala Val Ala Leu 100 105 110

Asp Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly
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Tyr Lys Asn Ile Cys Lys Val Val Glu Val Gly Ser Lys Ile Tyr Val
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Asp Asp Gly Leu Ile Ser Leu Gln Val Lys Gln Lys Gly Ala Asp Phe 180 185 190

Leu Val Thr Glu Val Glu Asn Gly Gly Ser Leu Gly Ser Lys Lys Gly
195 200 205

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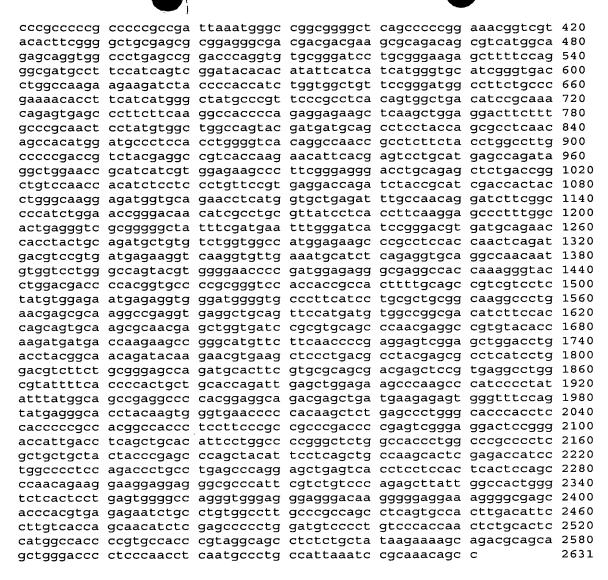
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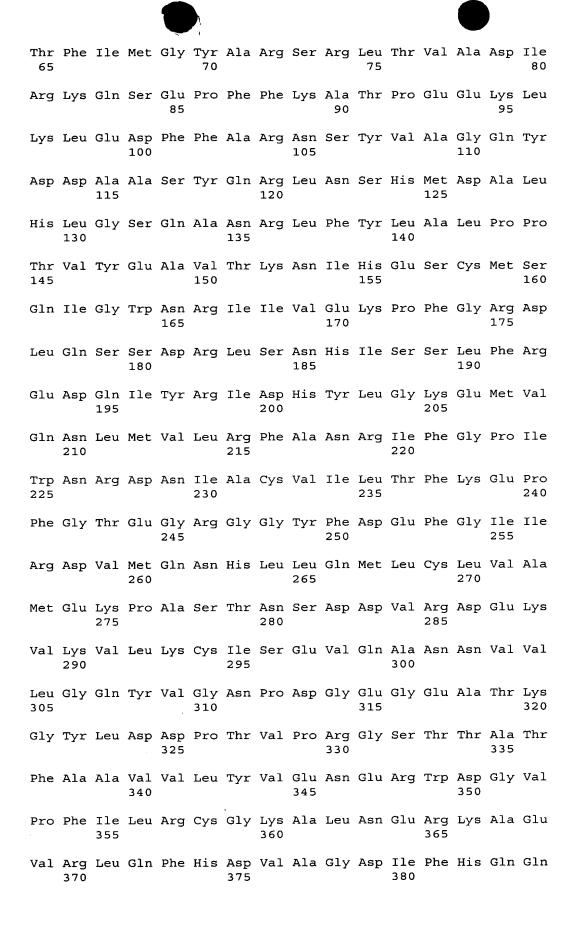
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Ser Val Asn Asn Cys Val Cys His Phe Ser Pro Leu Lys Ser Asp Gln 85 90 95

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His Val Asp Gly Phe Ile Ala Asn Val Ala His Thr Phe Val Val Asp 115 120 125

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His Val Ile Asp Gly Glu Lys Thr Ile Ile Gln Asn Pro Thr Asp Gln 195 200 205

Gln Lys Lys Asp His Glu Lys Ala Glu Phe Glu Val His Glu Val Tyr 210 215 220

Ala Val Asp Val Leu Val Ser Ser Gly Glu Gly Lys Ala Lys Asp Ala 225 230 235 240



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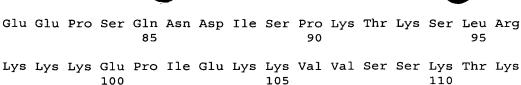
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Cys Asn Pro Ser Glu Ala Ala Ser Glu Glu Ser Asn Ser Glu Ile Glu
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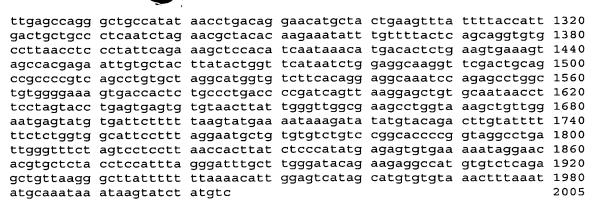
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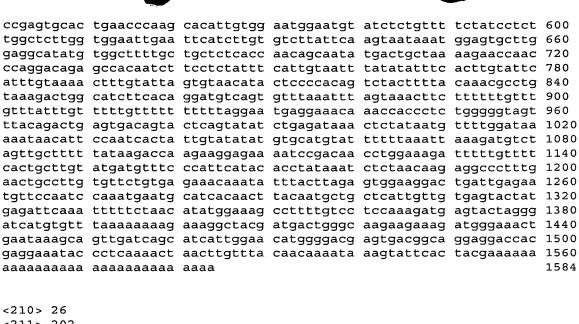


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<223> excision repair cross-complementing rodent repair
 deficiency, complementation group 1 (ERCC1) cDNA

<400> 27 ccaagaccag caggtgaggc ctcgcggcgc tgaaaccgtg aggcccggac cacaggctcc 60 agatggaccc tgggaaggac aaagaggggg tgccccagcc ctcagggccg ccagcaagga 120 agaaatttgt gatacccctc gacgaggatg aggtccctcc tggagtggcc aagcccttat 180 tccgatctac acagagcctt cccactgtgg acacctcggc ccaggcggcc cctcagacct 240 acgccgaata tgccatctca cagcctctgg aaggggctgg ggccacgtgc cccacagggt 300 cagagecect ggeaggagag acgeecaace aggeeetgaa acceggggea aaateeaaca 360 gcatcattgt gagccctcgg cagaggggca atcccgtact gaagttcgtg cgcaatgtgc 420 cctgggaatt tggcgacgta attcccgact atgtgctggg ccagagcacc tgtgccctgt 480 tecteageet eegetaceae aacetgeace eagactacat eeatgggegg etgeagagee 540 tggggaagaa cttcgccttg cgggtcctgc ttgtccaggt ggatgtgaaa gatccccagc 600 aggccctcaa ggagctggct aagatgtgta tcctggccga ctgcacattg atcctcgcct 660 ggagcccga ggaagctggg cggtacctgg agacctacaa ggcctatgag cagaaaccag 720 cggacctcct gatggagaag ctagagcagg acttcgtctc ccgggtgact gaatgtctga 780 ccaccgtgaa gtcagtcaac aaaacggaca gtcagaccct cctgaccaca tttggatctc 840 tggaacagct catcgccgca tcaagagaag atctggcctt atgcccaggc ctgggccctc 900 agaaagcccg gaggctgttt gatgtcctgc acgagccctt cttgaaagta ccctgatgac 960 cccagctgcc aaggaaaccc ccagtgtaat aataaatcgt cctcccaggc caggctcctg 1020 ctggc

<210> 28

<211> 297

<212> PRT

<213> Homo sapiens

<220>

<223> excision repair cross-complementing rodent repair
 deficiency, complementation group 1 (ERCC1)

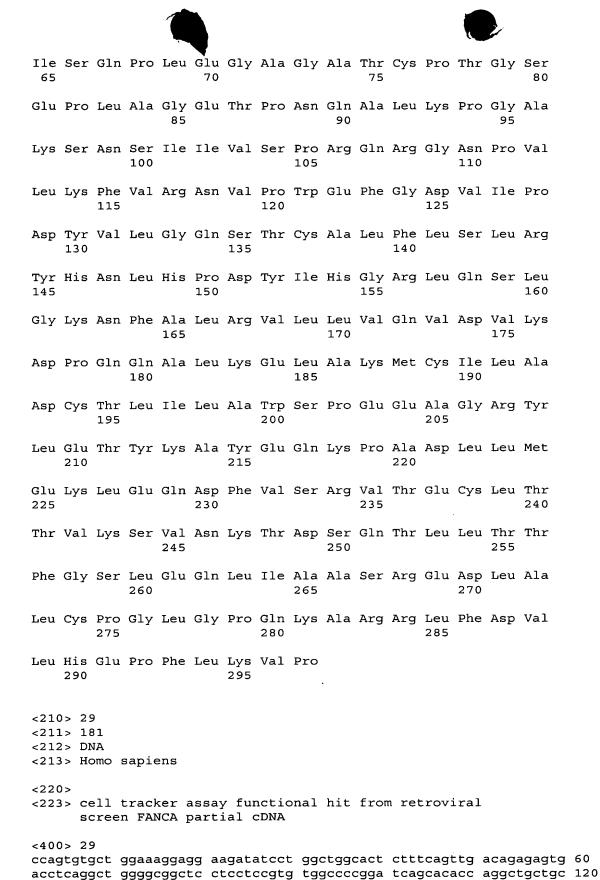
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Met Asp Pro Gly Lys Asp Lys Glu Gly Val Pro Gln Pro Ser Gly Pro

Pro Ala Arg Lys Lys Phe Val Ile Pro Leu Asp Glu Asp Glu Val Pro 20 25 30

Pro Gly Val Ala Lys Pro Leu Phe Arg Ser Thr Gln Ser Leu Pro Thr 35 40 45

Val Asp Thr Ser Ala Gln Ala Ala Pro Gln Thr Tyr Ala Glu Tyr Ala
50 55 60



181

ctttcgcttt ttacagtctt ctctcctact tccatgaaga cgcggctttc cagcacagtg 180

g



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<210> 30
<211> 603
<212> DNA
<213> Homo sapiens
<223> cell tracker assay functional hit from retroviral
      screen DDX9 partial cDNA
<400> 30
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cccctaccac cwcctcqctg gaatccccca gatcctctgt agcctccact aggccctctg 120
tagtctcctc cagagttgcc tctaaagcca cctcgggaga ctcctctata gcctccacca 180
acacetgeae catateetge eegaaaggag ttggegetge caceatagee teegetacea 240
tageeteeae tgetatagee acegeatage etecaceaet gtaactagaa eeteceette 300
tatatccgct tccattgtcg tatcgggcca tcttgggagg acgtggacca tctccatgcc 360
gtgtactgcc aatcataagg ttgataccag cagctgaggg tctagagatc tgacggatca 420
tgttcagcat acgttcattt acggggtcca actggctgat gatagcaggt tgtttggtta 480
cttcaacaac caaagcctcc atggctgccc ggagaccagt gatacaggca gcagcttcat 540
gagatatttg cagtttaatc cagtcatcta caagcacaat ctgcccactt tccagcacag 600
tgg
<210> 31
<211> 145
<212> DNA
<213> Homo sapiens
<220>
<223> cell tracker assay functional hit from retroviral
      screen IGF1R partial cDNA
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gcatcgatat ccacagctgc aaccacgagg ctgagaagct gggctgcagc gcctccaact 120
tcqtctttqc tttccagcac agtgg
                                                                   145
<210> 32
<211> 269
<212> DNA
<213> Homo sapiens
<220>
<223> cell tracker assay functional hit from retroviral
      screen UBEV2V1 partial cDNA
<400> 32
ccaqtgtgct ggaaaggtgc ttctgggtat ttaggtccac attctatttt aaggctgtat 60
attcqgtttt cataaattgt tcttggaggc ccaattatca tccctgtcca tcttgtaaga 120
tqtcatqtct tcqtcatctt ctagacccca gctaactgtg ccatctccta ctcctttctg 180
gccttcttcg agattcctcc aacagtcgga aattgcgagg gactttatac atcccgagcc 240
                                                                   269
cgtggtggct gccctttcca gcacactgg
<210> 33
<211> 499
<212> DNA
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<213> Homo sapiens





<220> <223> cell tracker assay functional hit from retroviral screen aldehyde dehydrogenase partial cDNA <400> 33 ccagtgtgct ggaaaggagc aaactcctct cactgctctc cacgtggcat ctttaataaa 60 agaggcaggg tttcctcctg gagtagtgaa tattgttcct ggttatgggc ctacagcagg 120 ggcagccatt tcttctcaca tggatataga caaagtagcc ttcacaggat caacagaggt 180 tggcaagttg atcaaagaag ctgccgggaa aagcaatctg aagagggtga ccctggagct 240 tggaggaaag agcccttgca ttgtgttagc tgatgccgac ttggacaatg ctgttgaatt 300 tgcacaccat ggggtattct accaccaggg ccagtgttgt atagccgcat ccaggatttt 360 tgtggaagaa tcaatttatg atgagttttg ttcgaaggag tgttgagcgg gctaagaacg 420 tatateettg gaaacateet etgaceecag gagteaetea aaggeeetea gattgacaag 480 gactttccag acacagtgg <210> 34 <211> 425 <212> DNA <213> Homo sapiens <220> <223> cell tracker assay functional hit from retroviral screen pyruvate dehydrogenase partial cDNA <400> 34 ccaqtqtqct qqaaaqqctq cccacttcca ccaccttgca gatgttcttg tagtccagcc 60 acaggatgtt ctcqtcacac ttttccatqt aggcqttatc cagcgtgatt ttgagagtgg 120 ctcccttctt cagctccacc tctgcagtgc cgctgccctt gatgagccca gttcggatct 180 caggtccttt agtgtctaga gccacagcaa cgggccggta gaggatgggg tcagaagcaa 240 agettteegt ggetgtgege acattettga tggteteege atggtaetea tgagtteeat 300 qaqaqaaqtt caqacqaqcc acattcattc caqacttaat catctccttc aacgtctcca 360 ctggatcggg aagctgggcc aatggtacag atgatgccag tgttccgggc tttccagcac 420 425 agtgg <210> 35 <211> 238 <212> DNA <213> Homo sapiens <220> <223> cell tracker assay functional hit from retroviral screen G6PD partial cDNA <220> <221> modified base <222> (1)..(238) <223> n = g, a, c or t<400> 35 ccaqtqtqct qqaaactttc caqttctcca tqqccaccan acacaqcatc tqcaqtaggt 60 ggttctgcat cacgtcccgg atgatcccaa attcatcgaa atagcccccg cgaccctcag 120 tgccaaaggg ctccttgaag gtgaggataa cgcaggcgat gttgtcccgg ttccanatgg 180 ggccgaagat cctgttggca aatctcagca ccatgaggtt ctctttccag cacagtgg <210> 36 <211> 491 <212> DNA

<213> Artificial Sequence





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<220>
<223> Description of Artificial Sequence:G3-2D8 sequence
      with C-terminus of GFP, partial BAP-1 sequence
<220>
<221> modified base
<222> (69)
<223> n = g, a, c or t
<400> 36
gagttegtga eegeegeegg gateactete ggeatggaeg agetgtacaa ggaggaggee 60
gccaaggeng gtggcagegg tggctccagt gtgctggaaa gctaagggca gagttggtgt 120
totgcacgtc atcotccgt catcotcata gtcatcotca tcatctgagt actgctgggg 180
tgggcggact ggaactcggc tgcggccac acctgccgcc aggtcttctt cctcctgcat 240
gggggacttg gcataattgt gattgtctag aaaggccggc agccgctgga caatgggagt 300
ggggttgggg tgaaccccat tgaggctgct gcctggaggc taccactagc ttgggtttgt 360
tgggagggct gtgggatggg gcttgtgcgc atgaaccagc cgcctcctcg caccatctgt 420
gtggttgccc tcagaggctg caggggccct gtttgcttcc agcaccagcg gggacctttc 480
cagcacagtg g
<210> 37
<211> 34
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence:G3-2D8 sequence
      with C-terminus of GFP, partial BAP-1 sequence
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu
                                 25
Glu Ser
<210> 38
<211> 16
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:BstXI linker
<400> 38
                                                                   16
ccagtgtgct ggaaag
<210> 39
<211> 16
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:BstXI linker
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<400> 39 ctttccagca cagtgg 16

<210> 40

<211> 136

<212> PRT

<213> Homo sapiens

<220>

<223> G1-2635 sequence, partial NP95 sequence

<400> 40

Ala Glu Gln Ser Cys Asp Gln Lys Leu Thr Asn Thr Asn Arg Ala Leu 1 5 10 15

Ala Leu Asn Cys Phe Ala Pro Ile Asn Asp Gln Glu Gly Ala Glu Ala 20 25 30

Lys Asp Trp Arg Ser Gly Lys Pro Val Arg Val Val Arg Asn Val Lys
35 40 45

Gly Gly Lys Asn Ser Lys Tyr Ala Pro Ala Glu Gly Asn Arg Tyr Asp 50 60

Gly Ile Tyr Lys Val Val Lys Tyr Trp Pro Glu Lys Gly Lys Ser Gly 65 70 75 80

Phe Leu Val Trp Arg Tyr Leu Leu Arg Arg Asp Asp Glu Pro Gly
85 90 95

Pro Trp Thr Lys Glu Gly Lys Asp Arg Ile Lys Lys Leu Gly Leu Thr
100 105 110

Met Gln Tyr Pro Glu Gly Tyr Leu Glu Ala Leu Ala Asn Arg Glu Arg
115 120 125

Glu Lys Glu Asn Ser Lys Arg Glu 130 135

<210> 41

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<223> G2-2F3 sequence, partial FANCA sequence

<400> 41

Arg Lys Ile Ser Trp Leu Ala Leu Phe Gln Leu Thr Glu Ser Asp Leu 1 5 10 15

Arg Leu Gly Arg Leu Leu Arg Val Ala Pro Asp Gln His Thr Arg
20 25 30

Leu Leu Pro Phe Ala Phe Tyr Ser Leu Leu Ser Tyr Phe His Glu Asp 35 40 45

Ala



<210> 42 <211> 552 <212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence:G3-2H6 sequence with C-terminus of GFP, partial DDX9 sequence

<400> 42

gagttegtga eegeegeegg gateactete ggeatggaeg agetgtacaa ggaggaggee 60 gccaaggccg gtggcagcgg tggctccagt gtgctggaaa gcgccacctc ctcttccctg 120 tecaaagtag ceagtteeat aggeeecet accaecteet egetggaate eeceagatee 180 tetgtageet ceaetaggee etetgtagte teetecagag ttgeetetaa agecaeeteg 240 ggagactect etatageete caccaacace tgeaceatat eetgeeegaa aggagttgge 300 gctgccacca tagcctccgc taccatagcc tccactgcta tagccaccgc atagcctcca 360 ccactgtaac tagaacctcc ccttctatat ccgcttccat tgtcgtatcg ggccatcttg 420 ggaggacgtg gaccatctcc atgccgtgta ctgccaatca taaggttgat accagcagct 480 gagggtctac agatctgacg gatcatgttc agcatacgtt catttacggg gtccaactgg 540 ctgatgatag ca

<210> 43

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: G3-2H6 sequence with C-terminus of GFP, partial DDX9 sequence

<400> 43

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 10 5

Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu

Glu Ser Ala Thr Ser Ser Ser Leu Ser Lys Val Ala Ser Ser Ile Gly 35 40

Pro Pro Thr Thr Ser Ser Leu Glu Ser Pro Arg Ser Ser Val Ala Ser

Thr Arg Pro Ser Val Val Ser Ser Arg Val Ala Ser Lys Ala Thr Ser 65 70 75

Gly Asp Ser Ser Ile Ala Ser Thr Asn Thr Cys Thr Ile Ser Cys Pro

Lys Gly Val Gly Ala Ala Thr Ile Ala Ser Ala Thr Ile Ala Ser Thr 100 105

Ala Ile Ala Thr Ala 115

<210> 44

<211> 38

<212> PRT

<213> Homo sapiens



<220>

<223> G3-2H2 1 sequence, partial IGF1R sequence

<400> 44

Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr Arg Ile
1 5 10 15

Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys Ser Ala 20 25 30

Ser Asn Phe Val Phe Ala 35

- <210> 45
- <211> 347
- <212> DNA
- <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:G3-2G2/2H2
 sequence with C-terminus of GFP, partial UBE2V1
 sequence

<400> 45

gagttcgtga ccgccgcgg gatcactctc ggcatggacg agctgtacaa ggaggaggcc 60 gccaaggccg gtggcagcgg tggctccagt gtgctggaaa ggtgcttctg ggtatttagg 120 tccacattct attttaaggc tgtatattcg gttttcataa attgttcttg gaggcccaat 180 tatcatcct gtccatcttg taagtgtcat gtcttcgtca tcttctagac cccagctaac 240 tgtgccatct cctactcctt tctggccttc ttcgagttct tccaacagtc ggaaattgcg 300 agggactttt actcccgagc ccgtggtggc tctttccagc acagtgg

- <210> 46
- <211> 75
- <212> PRT
- <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:G3-2G2/2H2
 sequence with C-terminus of GFP, partial UBE2V1
 sequence

<400> 46

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 1 5 10 15

Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu 20 25 30

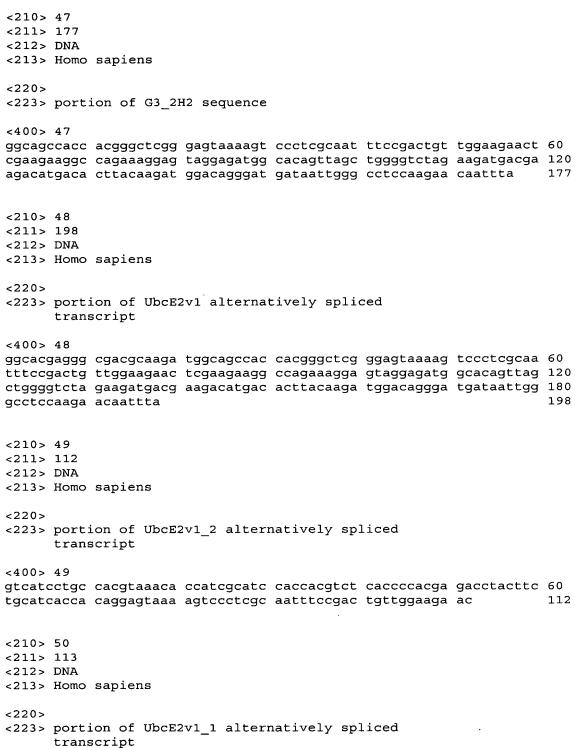
Glu Arg Cys Phe Trp Val Phe Arg Ser Thr Phe Tyr Phe Lys Ala Val 35 40 45

Tyr Ser Val Phe Ile Asn Cys Ser Trp Arg Pro Asn Tyr His Pro Cys
50 55 60

Pro Ser Cys Lys Cys His Val Phe Val Ile Phe 65 70 75



<400> 50



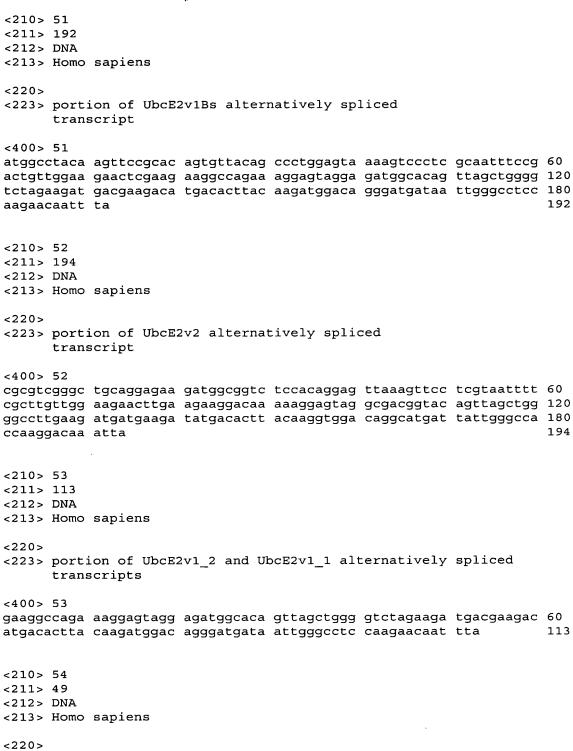
aagcgtctta cctgaagtca caaagcaaac tgagtgatga aggaagactt gaacctagaa 60

aatttcactg caaagggagt aaaagtccct cgcaatttcg actgttggaa gaa



<223> portion of G3_2H2 sequence

cgaatataca gccttaaaat agaatgtgga cctaaatacc cagaagcac



49



<210> 55

<211> 60

<212> DNA

<213> Homo sapiens

<220>

<223> portion of UbcE2v1, UbcE2v1_2, UbcE2v1_1 and UbcE2v1Bs
 alternatively spliced transcripts

4005 55

cgaatataca gccttaaaat agaatgtgga cctaaatacc cagaagcacc cccctttgta 60

<210> 56

<211> 60

<212> DNA

<213> Homo sapiens

<220>

<223> portion of UbcE2v2 alternatively spliced
 transcript

<400> 56

agaatatata gcctgaaagt agaatgtgga cctaaatacc cagaagctcc tccgtcagtt 60

<210> 57

<211> 225

<212> PRT

<213> Homo sapiens

<220>

<223> Uch-13 sequence

<400> 57

Met Glu Gly Gln Arg Trp Leu Pro Leu Glu Ala Asn Pro Glu Val Thr 1 5 10 15

Asn Gln Phe Leu Lys Gln Leu Gly Leu His Pro Asn Trp Gln Phe Val 20 25 30

Asp Val Tyr Gly Met Asp Pro Glu Leu Leu Ser Met Val Pro Arg Pro 35 40 45

Val Cys Ala Val Leu Leu Phe Pro Ile Thr Glu Lys Tyr Glu Val
50 55 60

Phe Arg Thr Glu Glu Glu Lys Ile Lys Ser Gln Gly Gln Asp Val 65 70 75 80

Thr Ser Ser Val Tyr Phe Met Lys Gln Thr Ile Ser Asn Ala Cys Gly 85 90 95

Thr Ile Gly Leu Ile His Ala Ile Ala Asn Asn Lys Asp Lys Met His
100 105 110

Phe Glu Ser Gly Ser Thr Leu Lys Lys Phe Leu Glu Glu Ser Val Ser 115 120 125

Met Ser Pro Glu Glu Arg Ala Arg Tyr Leu Glu Asn Tyr Asp Ala Ile 130 135 140





Arg Val Thr His Glu Thr Ser Ala His Glu Gly Gln Thr Glu Ala Pro 145 150 155 160

Ser Ile Asp Glu Lys Val Asp Leu His Phe Ile Ala Leu Val His Val 165 170 175

Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Lys Pro Phe Pro Ile Asn 180 185 190

His Gly Glu Thr Ser Asp Glu Thr Leu Leu Glu Asp Ala Ile Glu Val

Cys Lys Lys Phe Met Glu Arg Asp Pro Asp Glu Leu Arg Phe Asn Ala 210 215 220

Ile 225

<210> 58

<211> 231

<212> PRT

<213> Homo sapiens

<220>

<223> portion of BAP-1

<400> 58

Met Asn Lys Gly Trp Leu Glu Leu Glu Ser Asp Pro Gly Leu Phe Thr
1 5 10 15

Leu Leu Val Glu Asp Phe Gly Val Lys Gly Val Gln Val Glu Glu Ile
20 25 30

Tyr Asp Leu Gln Ser Lys Cys Gln Gly Pro Val Tyr Gly Phe Ile Phe 35 40 45

Leu Phe Lys Trp Ile Glu Glu Arg Arg Ser Arg Arg Lys Val Ser Thr 50 55 60

Leu Val Asp Asp Thr Ser Val Ile Asp Asp Asp Ile Val Asn Asn Met 65 70 75 80

Phe Phe Ala His Gln Leu Ile Pro Asn Ser Cys Ala Thr His Ala Leu 85 90 95

Leu Ser Val Leu Leu Asn Cys Ser Ser Val Asp Leu Gly Pro Thr Leu 100 105 110

Ser Arg Met Lys Asp Phe Thr Lys Gly Phe Ser Pro Glu Ser Lys Gly
115 120 125

Tyr Ala Ile Gly Asn Ala Pro Glu Leu Ala Lys Ala His Asn Ser His 130 135 140

Ala Arg Pro Glu Pro Arg His Leu Pro Glu Lys Gln Asn Gly Leu Ser 145 150 155 160

Ala Val Arg Thr Met Glu Ala Phe His Phe Val Ser Tyr Val Pro Ile 165 170 175





Thr Gly Arg Leu Phe Glu Leu Asp Gly Leu Lys Val Tyr Pro Ile Asp 180 185 190

His Gly Pro Trp Gly Glu Asp Glu Glu Trp Thr Asp Lys Ala Arg Arg 195 200 205

Val Ile Met Glu Arg Ile Gly Leu Ala Thr Ala Gly Glu Pro Tyr His 210 215 220

Asp Ile Arg Phe Asn Leu Met 225 230

<210> 59

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:poly Gly flexible linker

<220>

<221> MOD RES

<222> (6)..(200)

<223> Gly residues from position 6 to 200 may be present or absent

<400> 59





Gly Gly Gly Gly Gly Gly Gly 195 200

<210> 60

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DEAD box conserved motif

<400> 60

Asp Glu Ala Asp